

Supplementary Information for:

Biophysical Regulation of Chromatin Architecture Instills a Mechanical Memory in Mesenchymal Stem Cells

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SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Persistence of chromatin condensation with short term DL (600s, 1Hz) depends on the magnitude of applied strain (red line: unstrained CM control, DL: 600s, 1Hz, $n = \sim 20$, *: $p < 0.05$ vs. CM control, +: $p < 0.05$ vs. 3%, α : $p < 0.05$ vs. 0s, mean \pm s.e.m.).

Supplemental Figure 2. Chromatin condensation correlates with an increase in nuclear mechanics and a decrease in in situ nuclear deformation. (A) Treatment with $MgCl_2 + CaCl_2$ for 30 minutes increases chromatin condensation (top) and the number of visible edges in DAPI stained nuclei (bottom, bar = 3 μm). (B) Increased CCP with addition of $MgCl_2 + CaCl_2$ ($n = \sim 20$ cells, *: $p < 0.05$ vs. 0 mM, +: $p < 0.05$ vs. 10 mM, mean \pm s.e.m.). (C) Nuclear aspect ratio (NAR) as a function of treatment and with applied scaffold stretch ($n = \sim 45$, *: $p < 0.05$ vs. 0%, +: $p < 0.05$ vs. 9%, \times : $p < 0.05$ vs. 0 mM, mean \pm s.e.m.). (D) Peri-nuclear stiffness measured by atomic force microscopy (AFM) increases with an increase in chromatin condensation in response to $MgCl_2 + CaCl_2$ treatment ($n = 10$, *: $p < 0.05$ vs. 0 mM, mean \pm s.d.).

Supplemental Figure 3. Normalized CCP (relative to unloaded MSCs) after treatment for 30 minutes with complete or size fractionated DL-conditioned media (red line: unloaded CM control, $n = \sim 20$, *: $p < 0.05$ vs. CM control, mean \pm s.e.m.).

Supplemental Figure 4. (A) CCP increases with the addition of exogenous ATP ($n = \sim 20$, *: $p < 0.05$ vs. 0 mM, mean \pm s.e.m.). (B) UTP addition increased CCP, whereas BzATP added at the same concentration had no effect on CCP ($n = \sim 20$, *: $p < 0.05$ vs. CM control, mean \pm s.e.m.).

Supplemental Figure 5. Degradation of ATP in DL-conditioned media. ATP released from MSCs after 600s of DL gradually degraded, and did so at a faster rate when cells were present (37°C, $n = \sim 3$, *: $p < 0.05$ vs. without cells, +: $p < 0.05$ vs. 30m, α : $p < 0.05$ vs. 1h, β : $p < 0.05$ vs. 2h, normalized to ATP levels after 600s DL, mean \pm s.d.).

Supplemental Figure 6. (A-C) Representative images of YAP staining with treatment; (A): CM control, (B): 1mM ATP for 30 min, (C): 3% DL at 1Hz for 30 min (red: YAP, green: actin, blue: nucleus). (D) Nuclear to cytoplasmic YAP ratio with the addition of ATP or application of DL for 30 min normalized to CM control ($n = \sim 15$, *: $p < 0.05$ vs. CM control, mean \pm s.d.). (E) Ratio of nuclear to cytoplasmic YAP with the application of DL for 30 min under control conditions or with apyrase (AP, 5U) or flufenamic acid (FFA: a hemichannel blocker) added to the media during loading. Data normalized to unloaded CM control (red line) ($n = \sim 15$, *: $p < 0.05$ vs. CM control, mean \pm s.d.).

Supplemental Figure 7. Alterations in CCP with short and long term dynamic loading and pre-treatment with various inhibitors; (A): EGTA (a calcium chelator), (B): CALP2 (CALP, an antagonist of Calmodulin), (C): Cyclosporine A (CYSP, a Calcineurin inhibitor), (D): BAPTA-AM (BATAM, a calcium chelator), (E): Ruthenium red (RR, a TRPV4 inhibitor), (F): GSK205 (G205,

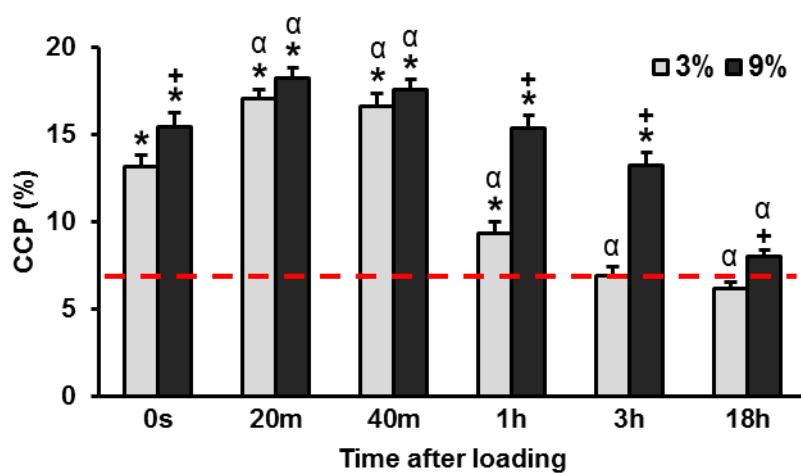
a TRPV4 antagonist), (**G**): GsMTx4 (GMT, a PIEZO ion channel inhibitor), (**H**): GdCl₃ (GC, a stretch-activated channel inhibitor), (**I**): PPADS (a P2 receptor antagonist). (DL: dynamic loading, red line: CM control, green line: DL 600s, blue line: DL 3h, n = ~20 per condition, *: p<0.05 vs. CM control, mean ± s.e.m.).

Supplemental Figure 8. Control studies showing no marked changes in (**A**) the baseline CCP (n= ~20) with the addition of pharmacological inhibitors for 600s or 3 hrs in unloaded conditions. (**B**) Nuclear deformation in MSCs subjected to static stretch with the addition of pharmacological inhibitors (n = ~50, CALP: CALP2, TG: thapsigargin, GC: GdCl₃, GSK: GSK205, *: p<0.05 vs. 0%, +: p<0.05 vs. 9% scaffold stretch, mean ± s.e.m.).

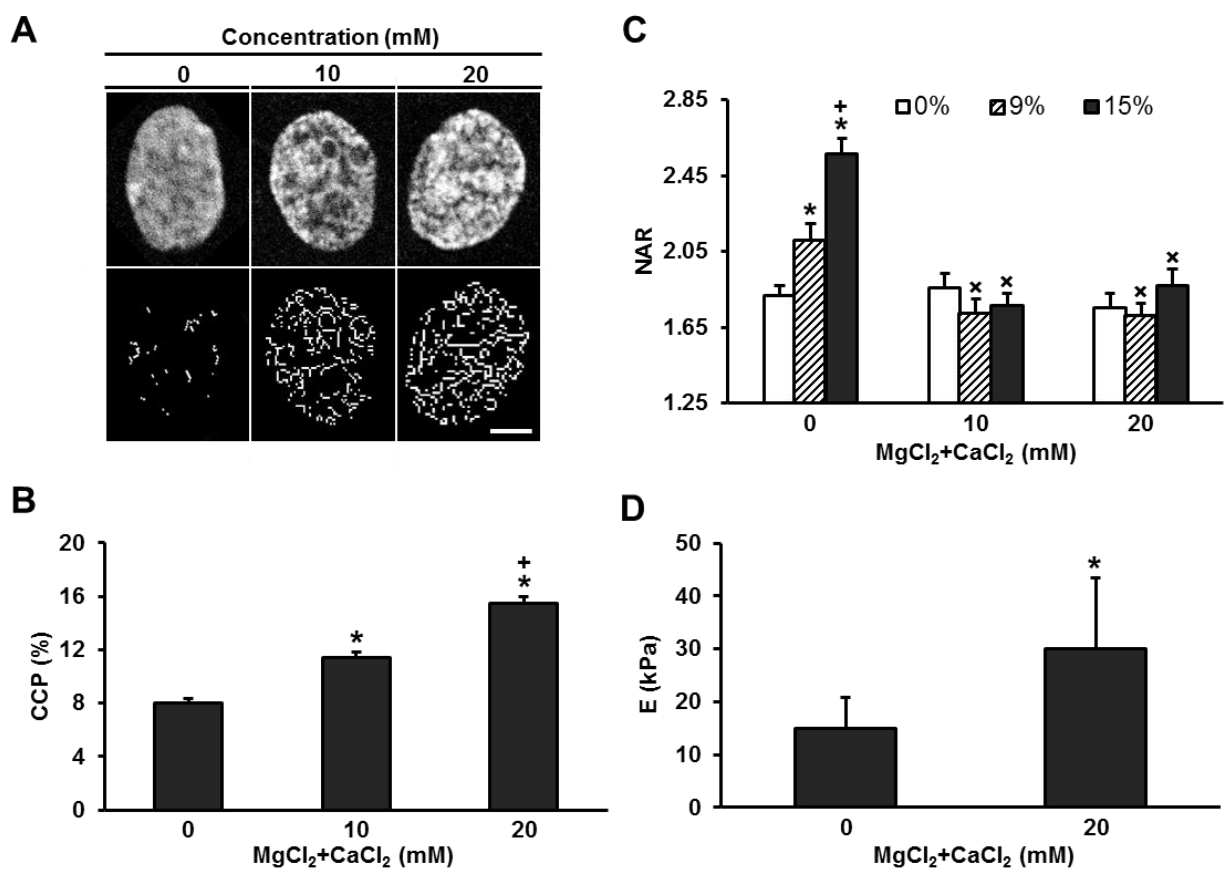
Supplemental Figure 9. TGF-β (**A**), SMC1A (**B**) and CTCF (**C**) gene expression normalized to CM control (red line: CM control, n = 9, from 3 replicates, *: p<0.05 vs. CM control, +: p<0.05 vs. a, ‡: p<0.05 vs. b, α: p<0.05 vs. c, mean ± s.e.m.).

Supplemental Figure 10. Change in aggrecan expression (AGG) as a function of the number of DL events and time after cessation of loading (n = ~ 3, *: p<0.05 vs. CM control (red line), +: p<0.05 vs. day 0, ‡: p<0.05 vs. day 3, mean ± s.d.).

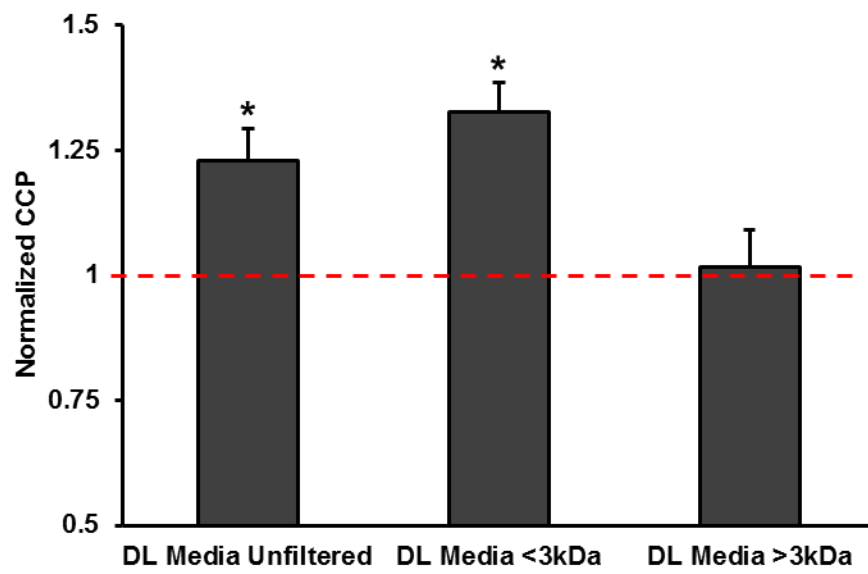
Supplemental Figure 1



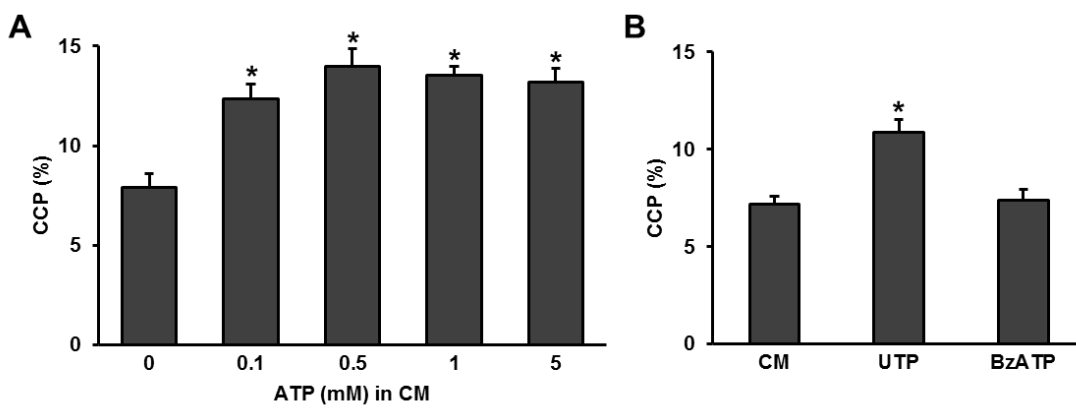
Supplemental Figure 2



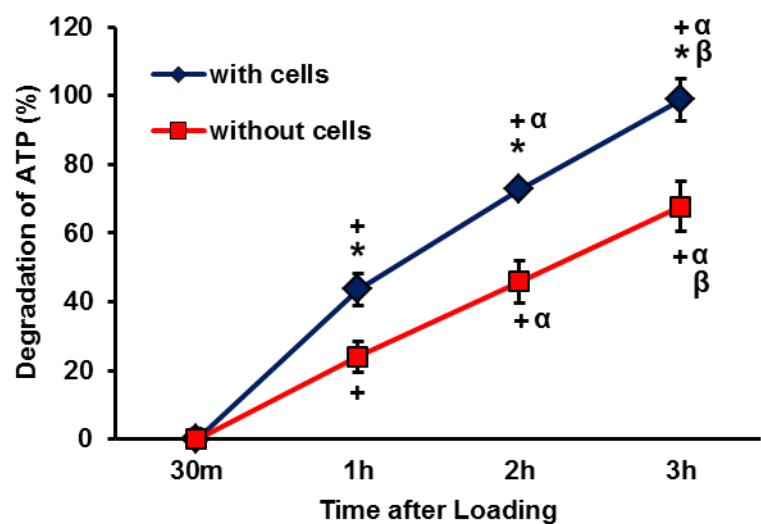
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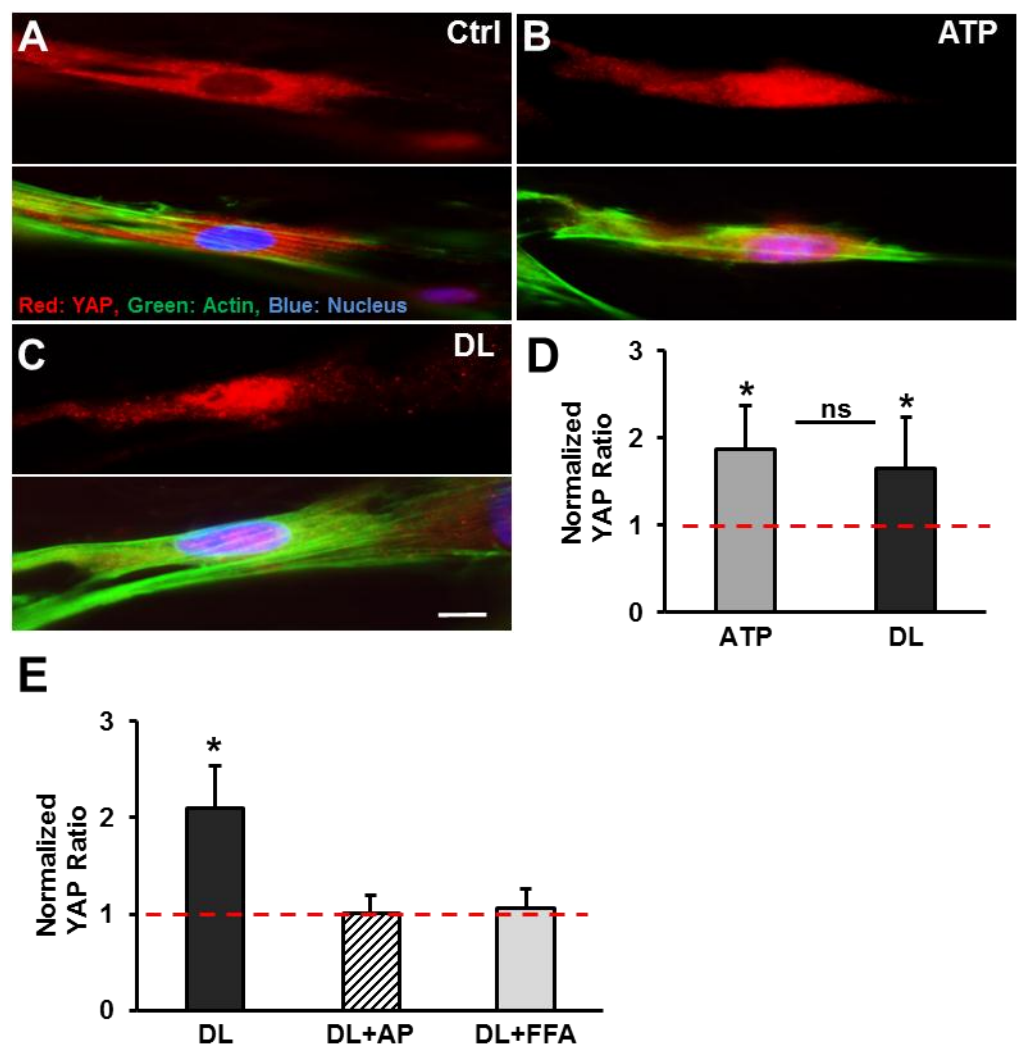
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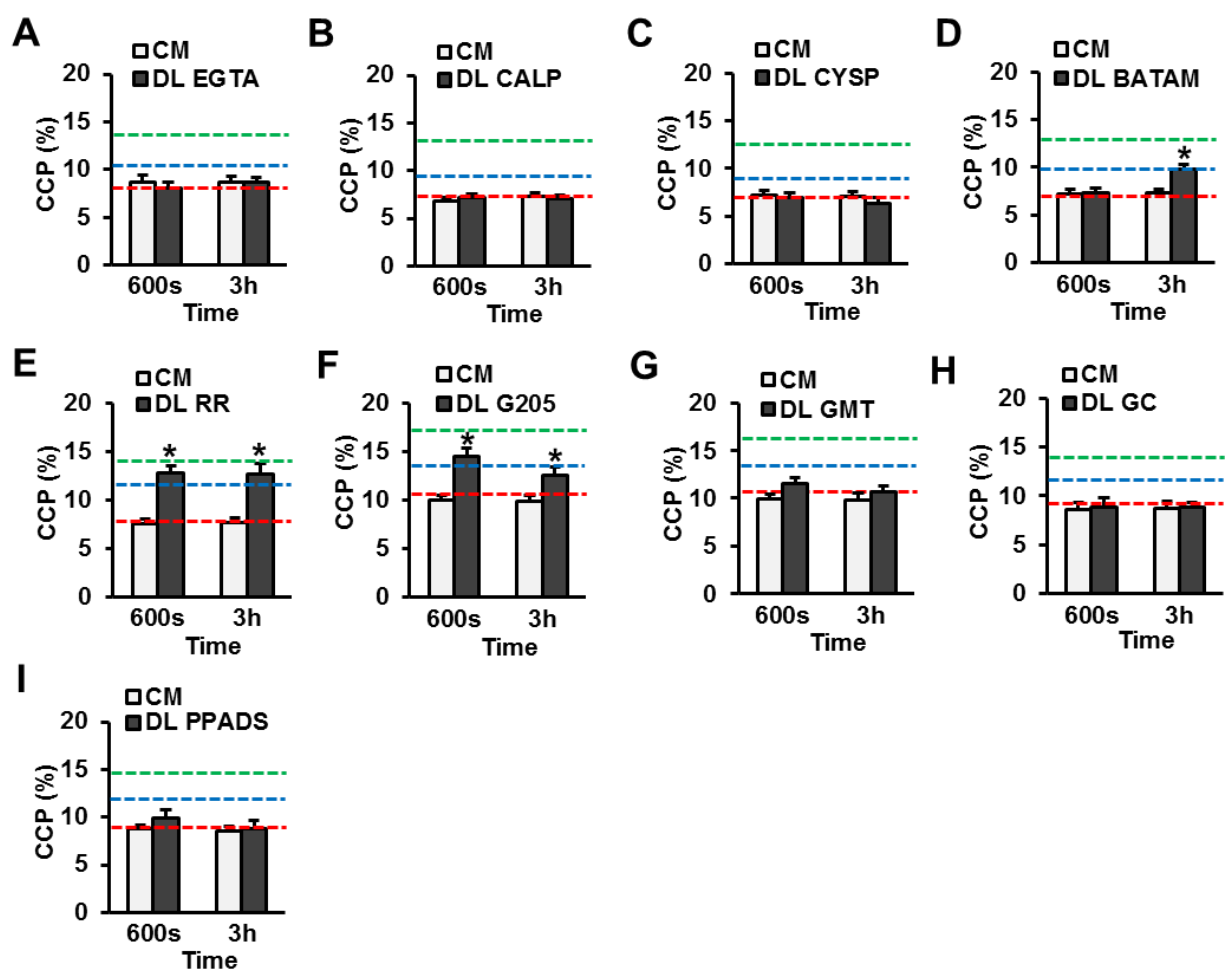
Supplemental Figure 5



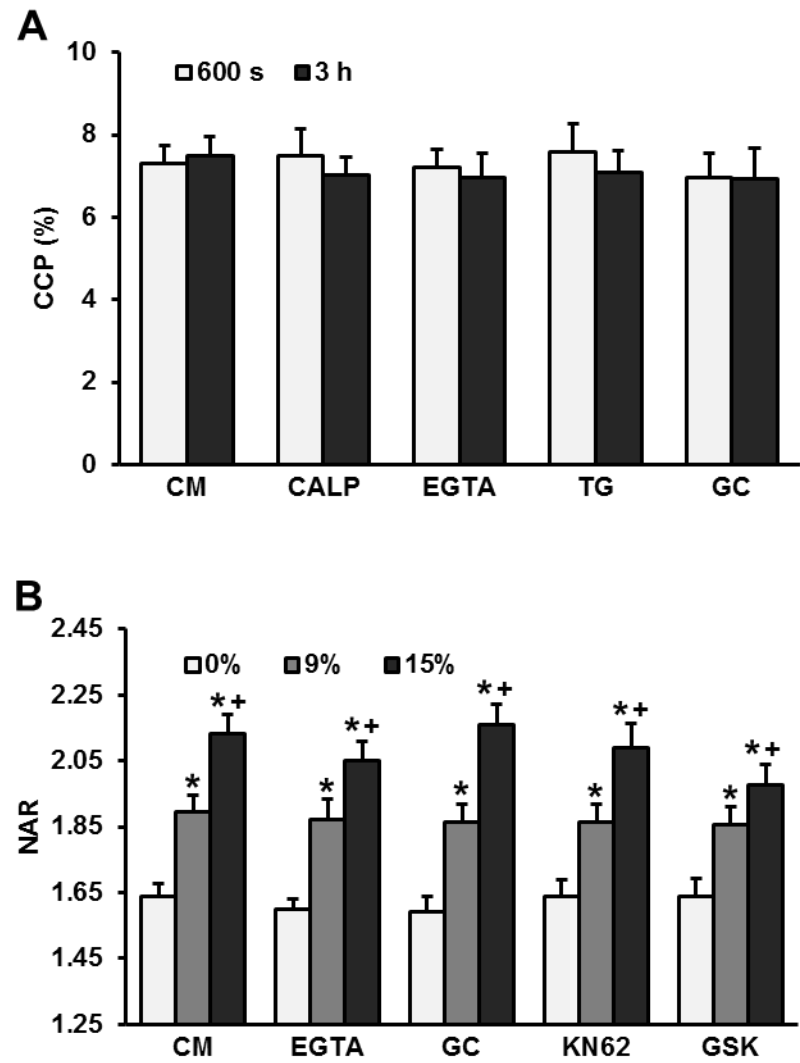
Supplemental Figure 6



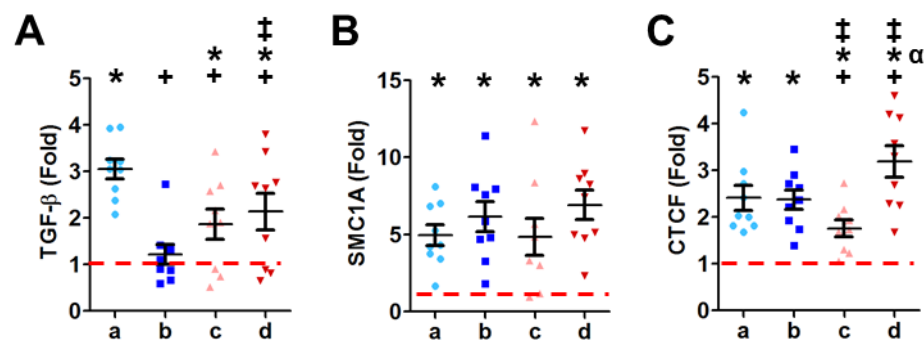
Supplemental Figure 7



Supplemental Figure 8



Supplemental Figure 9



Supplemental Figure 10

